

## Complete mitochondrial genome of *Schizothorax davidi* (Teleostei: Cypriniformes: Cyprinidae)

Shuo Feng, Zhifang An, Yue Wang and Jian Liang

State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, China

### ABSTRACT

This study provides a mitochondrial complete genome of *Schizothorax davidi*. The complete genome is 16,576 bp in length with an A+T content of 54.9%, which contains 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. The phylogenetic analysis indicated that *S. davidi* is closely related to *Schizothorax lissolabiatu*s. These results contribute to explore the adaptation strategy of *S. davidi* on the conditions of Qinghai-Tibet Plateau.

### ARTICLE HISTORY

Received 5 May 2019  
Accepted 31 July 2019

### KEYWORDS

*Schizothorax davidi*;  
mitochondrial genome;  
phylogenetic analysis

*Schizothorax davidi* belongs to the genus *Schizothorax*, within the subfamily *Schizothoracinae* (Cypriniformes, Cyprinidae), which was mainly distributed in the Jialing River and Minjiang River of the upstream of the Yangtze River (Ding 1994). China is the country with the largest distribution of *Schizothoracinae* fishes in the world (Wu and Wu 1991), and the germplasm resources have become a research hotspot.

In the last few years, some research of the phenotypic, physiological and molecular level (Qi et al. 2008; Zhao et al. 2008), but there was lack of the genomic information of the *Schizothoracinae* fishes. Therefore, establishing a complete mitochondrial genome sequence will contribute to explore the adaptation strategy of *S. davidi* on the conditions of Qinghai-Tibet Plateau.

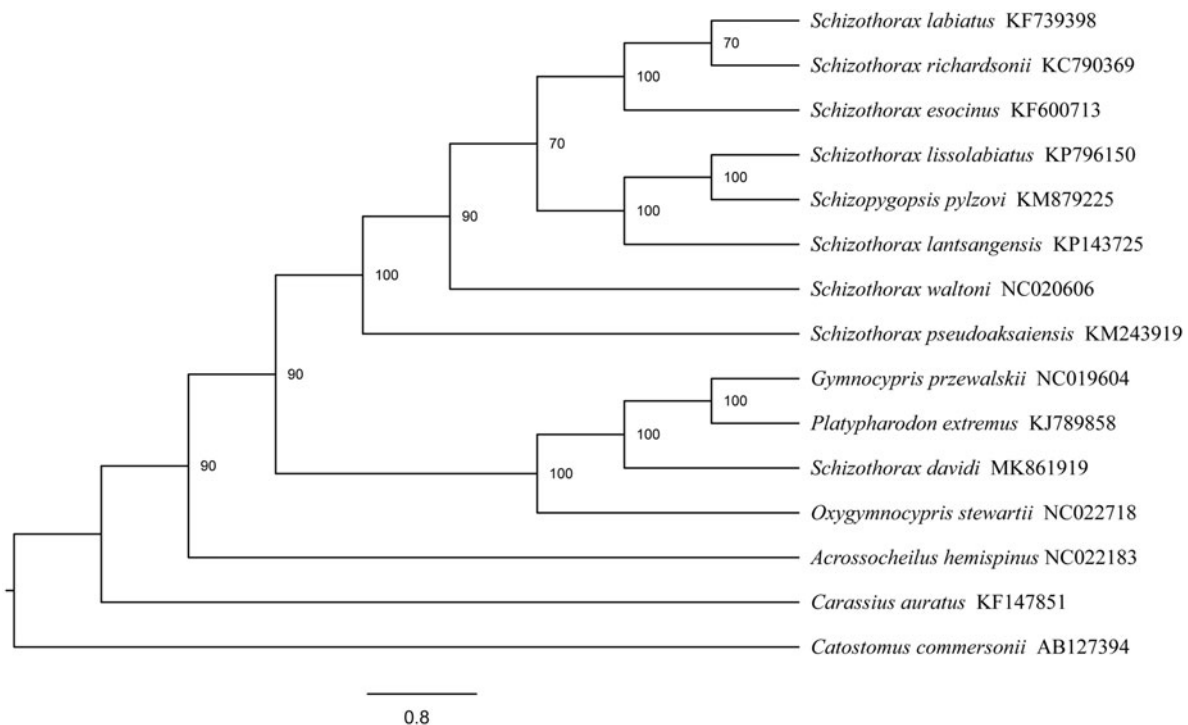


Figure 1. The maximum likelihood tree of the *Schizothorax davidi* and 14 other species with GenBank accession numbers.

In this study, *S. davidi* were collected from the Ruoergai County (Gansu, China; 102°37'E, 34°05'N) and voucher specimens (ZK-Ruoergai-001) were deposited at the Museum of State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University. The sample was frozen in liquid nitrogen immediately after collection and stored at  $-80^{\circ}\text{C}$ . The complete mitogenome sequence of *S. davidi* was deposited into GenBank database with accession number (MK861919). The whole length of the mitogenome of *S. davidi* is 16,576 bp, with an A + T content of 54.9%. The whole mitogenome contains 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes.

We constructed a phylogenetic tree (Figure 1) by RAxML 8.1.17 (Stamatakis 2014) to represent the phylogenetic relationships between *S. davidi* and other Schizothorax species. The results demonstrate that *S. davidi* had the highest homology with *Schizothorax lissolabiatus*, followed by *Schizothorax lantsangensis* (Figure 1).

### Disclosure statement

No potential conflict of interest was reported by the authors.

### Funding

This work was supported by the Project of Qinghai Science and Technology Department [2016-ZJ-940Q & 2016-ZJ-Y01] and the Open Project of State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University [2017-ZZ-01]. Dr. Shuo Feng was supported by '1000 Talent' programs of Qinghai Province.

### References

- Ding RH. 1994. The fishes of Sichuan, China. Chengdu: Sichuan Publishing House of Science and Technology.
- Qi DL, Chao Y, Guo SC, Zhao XQ. 2008. Genetic structure of five Huanghe schizothoracin *Schizopygopsis pylzovi* populations based on mtDNA control region sequences. *Acta Zool Sin.* 54: 972–980.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30: 1312–1313.
- Wu YF, Wu CZ. 1991. Fishes in the Qinghai-Tibet Plateau. Chengdu: Sichuan Science and Technology Publishing House; p. 149–233.
- Zhao XQ, Qi DL, Yang J. 2008. Study of the molecule evolution and adaptation of typical aboriginal animals in Qinghai-Tibetan Plateau. Beijing: Science Publishing Company; p. 5–12.